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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/846,456	05/02/2001	Marie-Francoise Rosier-Montus	ST00015 US NP	1457
5487	7590	07/31/2007	EXAMINER	
ROSS J. OEHLER			SULLIVAN, DANIEL M	
SANOFI-AVENTIS U.S. LLC			ART UNIT	PAPER NUMBER
1041 ROUTE 202-206				1636
MAIL CODE: D303A				
BRIDGEWATER, NJ 08807				
NOTIFICATION DATE		DELIVERY MODE		
07/31/2007		ELECTRONIC		

Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Notice of the Office communication was sent electronically on above-indicated "Notification Date" to the following e-mail address(es):

USPatent.E-Filing@sanofi-aventis.com
andrea.ryan@sanofi-aventis.com

Office Action Summary	Application No.	Applicant(s)	
	09/846,456	ROSIER-MONTUS ET AL.	
	Examiner	Art Unit	
	Daniel M. Sullivan	1636	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --
Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).

Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1) Responsive to communication(s) filed on 12 July 2007.
 2a) This action is **FINAL**. 2b) This action is non-final.
 3) Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4) Claim(s) 1,3,7-12,33-36 and 57-60 is/are pending in the application.
 4a) Of the above claim(s) _____ is/are withdrawn from consideration.
 5) Claim(s) _____ is/are allowed.
 6) Claim(s) 1,3,33-36 and 57-60 is/are rejected.
 7) Claim(s) 7-12 is/are objected to.
 8) Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9) The specification is objected to by the Examiner.
 10) The drawing(s) filed on _____ is/are: a) accepted or b) objected to by the Examiner.
 Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
 Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
 11) The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12) Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
 a) All b) Some * c) None of:
 1. Certified copies of the priority documents have been received.
 2. Certified copies of the priority documents have been received in Application No. _____.
 3. Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) <input checked="" type="checkbox"/> Notice of References Cited (PTO-892)	4) <input type="checkbox"/> Interview Summary (PTO-413)
2) <input type="checkbox"/> Notice of Draftsperson's Patent Drawing Review (PTO-948)	Paper No(s)/Mail Date. _____
3) <input type="checkbox"/> Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date _____	5) <input type="checkbox"/> Notice of Informal Patent Application
	6) <input checked="" type="checkbox"/> Other: <u>See Continuation Sheet</u> .

Continuation of Attachment(s) 6). Other: SEQUENCE SEARCH RESULTS 09/846,456.

DETAILED ACTION

This Office Action is a reply to the Paper filed 12 July 2007 in response to the Non-Final Office Action mailed 14 February 2007. Claims 1-3, 5-14, 33-38, 57-60 were considered in the 14 February Office Action. Claims 2, 5, 6, 37 and 38 were cancelled in the 12 July Paper. Claims 1, 3, 7-12, 33-36 and 57-60 are pending and under consideration. Finality of the previous Office Action is withdrawn in view of the new grounds for rejection set forth herein below.

Response to Amendment and Arguments

Rejection of claims 2, 5, 6, 37 and 38 is rendered moot by the cancellation thereof.

Claim Rejections - 35 USC § 112

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Rejection of claim 10 is rejected under 35 U.S.C. 112, second paragraph, as being indefinite in reciting, “ranging from nucleotide 1 at position -1” is withdrawn in view of the claim amendment.

New Grounds

Claim Objections

Claim 57 is objected to under 37 CFR 1.75(c), as being of improper dependent form for failing to further limit the subject matter of a previous claim. Applicant is required to cancel the claim(s), or amend the claim(s) to place the claim(s) in proper dependent form, or rewrite the

claim(s) in independent form. Claim 57 is directed to the isolated nucleic acid of claim 1, comprising at least 20 consecutive nucleotides of the sequence SEQ ID NO: 3 or the complement of SEQ ID NO: 3. Claim 1 is directed to an isolated nucleic acid comprising 500 or more consecutive nucleotides of SEQ ID NO: 1 or the complement of SEQ ID NO: 1.

As shown in the alignment of SEQ ID NO: 1 and SEQ ID NO: 3 attached hereto (us-09-846-456a-1.rnpbm, RESULT 7; page 8), SEQ ID NO: 3 comprises all but the final 338 bases of SEQ ID NO: 1. Therefore, any sequence comprising 500 or more consecutive nucleotides of SEQ ID NO: 1 must, at a minimum, comprise 162 bases of SEQ ID NO: 3. Therefore, all sequences within the scope of claim 1 must comprise more than 20 bases of SEQ ID NO: 3 and, consequently, claim 57 fails to further limit the subject matter of claim 1.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.

Claims 1, 3, 33-36 and 57-60 are rejected under 35 U.S.C. 102(a) as being anticipated by NCBI Entrez Nucleotide Database entry AC012230.2 (19 November 1999),
<http://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?val=6454033>, downloaded 25 July 2007 as evidenced by Osoegawa et al. (2001) *Genome Res.* 11:483-496.

Claim 1 is directed to an isolated nucleic acid comprising a polynucleotide having 500 or more consecutive nucleotides of the nucleotide sequence SEQ ID NO: 1 and claim 3 is directed

to an isolated nucleic acid comprising a polynucleotide having at least 200 consecutive nucleotides of the sequence SEQ ID NO: 3. Claim 57 is directed to the nucleic acid of claim 1, wherein the nucleic acid comprises at least 20 consecutive nucleotides of SEQ ID NO: 3.

The AC012230 entry teaches a nucleic acid comprising a 540 base sequence that is identical to nucleotides 2130-2670 of SEQ ID NO: 1 and 3. (See the alignment of SEQ ID NO: 3 with the AC012230 entry on the attached sequence search results (us-09-846-456a-3.oli.rge, RESULT 11). Note that the sequence at nucleotides 2130-2670 of SEQ ID NO: 1 is identical to the sequence of SEQ ID NO: 3 (see us-09-846-456a-1.rnpbm, RESULT 7; page 8 of the attached sequence search). Also note that the alignment on the sequence search is numbered according to version 3 of the AC012230 entry while the cited art is version 2 (i.e., AC012230.2). The corresponding sequence begins at 2703 and continues through 3243 of the AC012230.2 sequence.

The AC012230 entry anticipates the limitations of the instant claims 1, 3 and 57. In addition, the AC012230 nucleic acid further comprises additional sequence which is "of interest" according to the limitations of claim 33 and would additionally comprise sequence that is in the sense and antisense orientation with respect to the promoter comprised by the nucleic acid, as well as sense and antisense sequences of interest comprised by the BAC vector itself, according to the limitations of claim 34. Claim 58 recites that the isolated nucleic acid further comprises 35 or more consecutive nucleotides of SEQ ID NO: 5 or the complement of SEQ ID NO: 5. This limitation is met by, for example, the sequence from 147555-147614 of the AC012230.2 sequence, which is 100% complementary to the sequence from nucleotide 100 to nucleotide 159 of SEQ ID NO: 5.

Finally, the AC012230 entry teaches that the sequence is comprised in an RP11 clone (a.k.a., RPC-11; see under "DEFINITION"). Osoegawa et al. teaches that RPCI-11 is a BAC library. (See especially page 492, second sentence of the "DISCUSSION".) In view of the fact that nucleic acids in BAC libraries are comprised within vectors and propagated in bacteria, the cloning vector of claims 35 and 36 and isolated host cell of claims 59 and 60 are inherent to the teaching of the nucleic acid comprised in an RP11 clone as disclosed in the AC012230.

Database entry AC012230, as evidenced by Osoegawa et al., teaches all of the limitations of the instant claims. Therefore, the claims are anticipated by the prior art.

Allowable Subject Matter

Claims 7-12 are objected to as being dependent upon a rejected base claim, but would be allowable if rewritten in independent form including all of the limitations of the base claim and any intervening claims.

Conclusion

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Daniel M. Sullivan whose telephone number is 571-272-0779. The examiner can normally be reached on Monday through Friday 6:30-3:00.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Joseph Woitach, Ph.D. can be reached on 571-272-0739. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Patent applicants with problems or questions regarding electronic images that can be viewed in the Patent Application Information Retrieval system (PAIR) (<http://pair>-

Art Unit: 1636

direct.uspto.gov) can now contact the USPTO's Patent Electronic Business Center (Patent EBC) for assistance. Representatives are available to answer your questions daily from 6 am to midnight (EST). The toll free number is (866) 217-9197. When calling please have your application serial or patent number, the type of document you are having an image problem with, the number of pages and the specific nature of the problem. The Patent Electronic Business Center will notify applicants of the resolution of the problem within 5-7 business days.

Applicants can also check PAIR to confirm that the problem has been corrected. The USPTO's Patent Electronic Business Center is a complete service center supporting all patent business on the Internet. The USPTO's PAIR system provides Internet-based access to patent application status and history information. It also enables applicants to view the scanned images of their own application file folder(s) as well as general patent information available to the public.

For all other customer support, please call the USPTO Call Center (UCC) at 800-786-9199.



Daniel M. Sullivan, Ph.D.

Primary Examiner

Art Unit 1636

SEQUENCE SEARCH RESULTS 09/846,456

us-09-846-456a-3.oli.rge

RESULT 11
AC012230

LOCUS AC012230 175064 bp DNA linear HTG 22-APR-2000
DEFINITION Homo sapiens clone RP11-1M10, WORKING DRAFT SEQUENCE, 39 unordered pieces.
ACCESSION AC012230.
VERSION AC012230.3 GI:7637254
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 175064)
AUTHORS Birren,B., Linton,L.; Nusbaum,C. and Lander,E.
TITLE Homo sapiens, clone RP11-1M10
JOURNAL Unpublished

REFERENCE 2 (bases 1 to 175064)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M., Baldwin,J., Barna,N., Beckerly,R., Boguslavkiy,L., Boukhalter,B., Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M., Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D., Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J., Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X., Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.

TITLE Direct Submission
JOURNAL Submitted (21-OCT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

COMMENT On Apr 22, 2000 this sequence version replaced gi:6454033.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information
Center project name: L2510
Center clone name: 1_M_10

----- Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 117571 bases at least Q40
Consensus quality: 145749 bases at least Q30
Consensus quality: 160940 bases at least Q20
Insert size: 185000; agarose-fp
Insert size: 171264; sum-of-contigs
Quality coverage: 2.9 in Q20 bases; agarose-fp
Quality coverage: 3.2 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 39 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1003: contig of 1003 bp in length

* 1004 1103: gap of 100 bp
* 1104 2634: contig of 1531 bp in length
* 2635 2734: gap of 100 bp
* 2735 4415: contig of 1681 bp in length
* 4416 4515: gap of 100 bp
* 4516 5785: contig of 1270 bp in length
* 5786 5885: gap of 100 bp
* 5886 7879: contig of 1994 bp in length
* 7880 7979: gap of 100 bp
* 7980 9686: contig of 1707 bp in length
* 9687 9786: gap of 100 bp
* 9787 12253: contig of 2467 bp in length
* 12254 12353: gap of 100 bp
* 12354 15228: contig of 2875 bp in length
* 15229 15328: gap of 100 bp
* 15329 17200: contig of 1872 bp in length
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* 17301 20131: contig of 2831 bp in length
* 20132 20231: gap of 100 bp
* 20232 22587: contig of 2356 bp in length
* 22588 22687: gap of 100 bp
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* 52719 56592: contig of 3874 bp in length
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* 56693 59635: contig of 2943 bp in length
* 59636 59735: gap of 100 bp
* 59736 63661: contig of 3926 bp in length
* 63662 63761: gap of 100 bp
* 63762 68437: contig of 4676 bp in length
* 68438 68537: gap of 100 bp
* 68538 71458: contig of 2921 bp in length
* 71459 71558: gap of 100 bp
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* 76889 76988: gap of 100 bp
* 76989 82113: contig of 5125 bp in length
* 82114 82213: gap of 100 bp
* 82214 88220: contig of 6007 bp in length
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* 88321 93499: contig of 5179 bp in length
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* 97902 98001: gap of 100 bp
* 98002 103016: contig of 5015 bp in length
* 103017 103116: gap of 100 bp
* 103117 109178: contig of 6062 bp in length
* 109179 109278: gap of 100 bp
* 109279 117307: contig of 8029 bp in length
* 117308 117407: gap of 100 bp
* 117408 124079: contig of 6672 bp in length
* 124080 124179: gap of 100 bp
* 124180 131281: contig of 7102 bp in length
* 131282 131381: gap of 100 bp
* 131382 138059: contig of 6678 bp in length
* 138060 138159: gap of 100 bp

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*    138160    145491: contig of 7332 bp in length
*    145492    145591: gap of 100 bp
*    145592    157391: contig of 11800 bp in length
*    157392    157491: gap of 100 bp
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                  /clone_lib="RPCI-11 Human Male BAC"
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                  /note="assembly_fragment"
misc_feature     1104..2634
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                  /note="assembly_fragment"
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misc_feature     63762..68437
                  /note="assembly_fragment"
misc_feature     68538..71458
                  /note="assembly_fragment"
                  clone_end:SP6
                  vector_side:left"

```

Query Match 18.7%; Score 541; DB 2; Length 175064;
Best Local Similarity 100.0%; Pred. No. 2.4e-294;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2130 TTTGTTTGTTCCTTTTTGTTGGCCTCCTCTCAATTATGAAGAGAAGCA 2189

Db 2903 TTTGTTGTTCTTTTGTGGCCTCCTCAATTATGAAGAGAAGCA 2962
 Qy 2190 GTAAGATGTTCCCTCGGGCCTCTGAGGGACCTGGGAGCTCAGGCTGGGAATCTCCAA 2249
 |||||||
 Db 2963 GTAAGATGTTCCCTCGGGCCTCTGAGGGACCTGGGAGCTCAGGCTGGGAATCTCCAA 3022
 Qy 2250 GGCAGTAGGTGCCTATCAAAAATCAAAGTCCAGGTTGTGGGGAAAACAAAAGCAGC 2309
 |||||||
 Db 3023 GGCAGTAGGTGCCTATCAAAAATCAAAGTCCAGGTTGTGGGGAAAACAAAAGCAGC 3082
 Qy 2310 CCATTACCCAGAGGACTGTCCGCCTCCCCCTACCCCGCCTAGGCCTTGAAGGAAAC 2369
 |||||||
 Db 3083 CCATTACCCAGAGGACTGTCCGCCTCCCCCTACCCCGCCTAGGCCTTGAAGGAAAC 3142
 Qy 2370 AAAAGACAAGACAAAATGATTGGCGCTTGAGGGAGATTAGCCTAGAGCTCTCTCCC 2429
 |||||||
 Db 3143 AAAAGACAAGACAAAATGATTGGCGCTTGAGGGAGATTAGCCTAGAGCTCTCTCCC 3202
 Qy 2430 CCAATCCCTCCCTCGGCTGAGGAAACTAACAAAGGAAAAAAATTGCGGAAAGCAGGA 2489
 |||||||
 Db 3203 CCAATCCCTCCCTCGGCTGAGGAAACTAACAAAGGAAAAAAATTGCGGAAAGCAGGA 3262
 Qy 2490 TTTAGAGGAAGCAAATTCCACTGGTGCCTTGGCTGCCGGAACGTGGACTAGAGAGTCT 2549
 |||||||
 Db 3263 TTTAGAGGAAGCAAATTCCACTGGTGCCTTGGCTGCCGGAACGTGGACTAGAGAGTCT 3322
 Qy 2550 GCGCGCAGCCCCGAGCCCAGCGCTTCCCGCGCTTCTAGGCCGGCGGGCCGGCGGG 2609
 |||||||
 Db 3323 GCGCGCAGCCCCGAGCCCAGCGCTTCCCGCGCTTCTAGGCCGGCGGGCCGGCGGG 3382
 Qy 2610 GAAGGGACGCAGACCGCGGACCCATAAGACACCTGCTGTACCTCCACCCACCCACC 2669
 |||||||
 Db 3383 GAAGGGACGCAGACCGCGGACCCATAAGACACCTGCTGTACCTCCACCCACCCACC 3442
 Qy 2670 C 2670
 |
 Db 3443 C 3443

45409-8464156474. 3443

RESULT 12
 AC012230/c
 LOCUS AC012230 175064 bp DNA linear HTG 22-APR-2000
 DEFINITION Homo sapiens clone RP11-1M10, WORKING DRAFT SEQUENCE, 39 unordered pieces.
 ACCESSION AC012230
 VERSION AC012230.3 GI:7637254
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 175064)
 AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
 TITLE Homo sapiens, clone RP11-1M10
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 175064)
 AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J.; Meldrim, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,

Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
 Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
 Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
 TITLE Direct Submission
 JOURNAL Submitted (21-OCT-1999) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 COMMENT On Apr 22, 2000 this sequence version replaced gi:6454033.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L2510
 Center clone name: 1_M_10
 ----- Summary Statistics
 Sequencing vector: M13; M77815; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 117571 bases at least Q40
 Consensus quality: 145749 bases at least Q30
 Consensus quality: 160940 bases at least Q20
 Insert size: 185000; agarose-fp
 Insert size: 171264; sum-of-contigs
 Quality coverage: 2.9 in Q20 bases; agarose-fp
 Quality coverage: 3.2 in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 39 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
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 * as soon as it is available and the accession number will
 * be preserved.
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 * 1004 1103: gap of 100 bp
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 * 2635 2734: gap of 100 bp
 * 2735 4415: contig of 1681 bp in length
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 * 5786 5885: gap of 100 bp
 * 5886 7879: contig of 1994 bp in length
 * 7880 7979: gap of 100 bp
 * 7980 9686: contig of 1707 bp in length
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 * 9787 12253: contig of 2467 bp in length
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 * 12354 15228: contig of 2875 bp in length
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 * 25808 28184: contig of 2377 bp in length
 * 28185 28284: gap of 100 bp
 * 28285 31338: contig of 3054 bp in length
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*    82114    82213: gap of 100 bp
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 Matches 394; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 7
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; Sequence 3, Application US/09846456
; Patent No. US20020146792A1
; GENERAL INFORMATION:
; APPLICANT: Rosier, Marie
; APPLICANT: Prades, Catherine
; APPLICANT: Lemoine, Cendrine
; APPLICANT: Naudin, Laurent
; APPLICANT: Denefle, Patrice
; APPLICANT: Duverger, Nicolas
; APPLICANT: Brewer, Bryan
; APPLICANT: Remaley, Alan
; APPLICANT: Fojo, Silvia
; TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modifying Its
; TITLE OF INVENTION: Activity and Therapeutic Uses
; FILE REFERENCE: 3806.0505
; CURRENT APPLICATION NUMBER: US/09/846,456
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/201,280
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 2893
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-846-456-3

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